

FIG. 1A

1	CTCTCTCAGCTTCAGAGGGAAAAAATGGTTGTAGATTTCTGGACTTGGGAGCAGACATT	60
1	M V V D F W T W E Q T F	12
61	TCAAGAACTAATCCAAGAGGCAAAACCCCGGGCCACATGGACGCTGAAGTTGGATGGCAA	120
13	Q E L I Q E A K P R A T W T L K L D G N	32
121	CCTTCAGCTAGACTGCCTGGCTCAAGGGTGAAGCAATACCAACAGAGAGCATTGCTG	180
33	L Q L D C L A Q G W K Q Y Q Q R A F G W	52
181	GTTCCGGTGTTCCTCCTGCCAGCGAAGTTGGGCTTCCGCCCAAGTGCAGATTCTGTGCCA	240
53	F R C S S C Q R S W A S A Q V Q I L C H	72
241	CACGTACTGGGAGCACTGGACATCCCAGGGTCAGGTGCGTATGAGGCTCTTTGGCCAAAG	300
73	T Y W E H W T S Q G Q V R M R L F G Q R	92
301	GTGCCAGAAGTGCTCCTGGTCCCAATATGAGATGCCTGAGTTCTCCTCGGATAGCACCAT	360
93	C Q K C S W S Q Y E M P E F S S D S T M	112
361	GAGGATTCTGAGCAACCTGGTGCAGCATATACTGAAGAAATACTATGGAAATGGCACGAG	420
113	R I L S N L V Q H I L K K Y Y G N G T R	132
421	GAAGTCTCCAGAAATGCCAGTAATCCTGGAAGTGTCCCTGGAAGGATCCCATGACACAGC	480
133	K S P E M P V I L E V S L E G S H D T A	152
481	CAATTGTGAGGCATGCACTTTGGGCATCTGTGGACAGGGCTTAAAAAGCTGCATGACAAA	540
153	N C E A C T L G I C G Q G L K S C M T K	172
541	GCCGTCCAAATCCCTACTCCCCACCTAAAGACTGGGAATTCCTCACCTGGAATTGGTGC	600
173	P S K S L L P H L K T G N S S P G I G A	192
601	TGTGTACCTCGCAAACCAAGCCAAGAACCAGTCAGCTGAGGCAAAAGAGGCTAAGGGGAG	660
193	V Y L A N Q A K N Q S A E A K E A K G S	212
661	TGGGTATGAGAAATTAGGGCCCAGTCGAGACCCAGATCCACTGAACATCTGTGTCTTTAT	720
213	G Y E K L G P S R D P D <u>P L N I C V F I</u>	232
721	TTTGCTGCTTGATTTATTGTAGTCAAATGCTTTACATCAGAATGATGAAAATAGGCTTG	780
233	<u>L L L V F I V V K C F</u> T S E	246
781	CCACTTTCTCTTATTTTAATTCATGGTAGTCAATGAACTGGCTGCCACTTTAATATAAC	840

FIG. 1B

841 TGAAAATTCATTTTGAGACCAAGCAGGATCAAGTTGTAGAATAAACACTGGTTTCCTAG 900
901 CCATCCTCTGAAAACAGTATGAAACATGACCAAGTACATAATGGATTTAGTAATAAATAT 960
961 TGTCTGAATTGCTAAAAAAAAAAAAAAAAAAG 989

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FIG. 2

1	ATGAGGGTTATAGAAGGGAAGGGCTTTGCCCAAGGTCTTCCTGATGTAAACTGGATCTTC	60
1	M R V I E G K G F A Q G L P D V N W I F	20
61	AACCCAGGTTCCGGTGTTCCTCCTGCCAGCGAAGTTGGGCTTCCGCCCAAGTGCAGATTC	120
21	N P G S G V P P A S E V G L P P K C R F	40
121	TGTGCCACACGTACTGGGAGCACTGGACATCCCAGGGTCAGGTGCCAGAAGTGCTCCTGG	180
41	C A T R T G S T G H P R V R C Q K C S W	60
181	TCCCAATATGAGATGCCTGAGTTCTCCTCGGATAGCACCATGAGGATTCTGAGCAACCTG	240
61	S Q Y E M P E F S S D S T M R I L S N L	80
241	GTGCAGCATATACTGAAGAAATACTATGGAAATGGCACGAGGAAGTCTCCAGAAATGCCA	300
81	V Q H I L K K Y Y G N G T R K S P E M P	100
301	GTAATCCTGGAAGTGTCCCTGGAAGGATCCCATGACACAGCCAATTGTGAGGCATGCACT	360
101	V I L E V S L E G S H D T A N C E A C T	120
361	TTGGGCATCTGTGGACAGGGCTTAAAAAGCTGCATGACAAAGCCGTCCAAATCCCTACTC	420
121	L G I C G Q G L K S C M T K P S K S L L	140
421	CCCCACCTAAAGACTGGGAATTCCTCACCTGGAATTGGTGCTGTGTACCTCGCAAACCAA	480
141	P H L K T G N S S P G I G A V Y L A N Q	160
481	GCCAAGAACCAGTCAGCTGAGGCAAAAGAGGCTAAGGGGAGTGGGTATGAGAAATTAGGG	540
161	A K N Q S A E A K E A K G S G Y E K L G	180
541	CCAGTCGAGACCCAGATCCACTGAACATCTGTGTCTTTATTTTGCTGCTTGTATTTATT	600
181	P S R D P D P L N I C V F I L L L V F I	200
601	GTAGTCAAATGCTTTACATCAGAA	624
201	V V K C F T S E	208

FIG. 3A

bmy_hpp13.fas	MVVDFTWEQ	TFQELIQEAK	PRATWTLKLD	GNLQLDCLAQ	GWKQYQORAF
pdb1qb0.A.-
bmy_hpp13.fas	GWFRCCSCQR	SWASAQVQIL	CHTYWEHWTS	QGQVRMRLFG	QRCQKCSWSQ
pdb1qb0.A.-VLRKSL	CHDEIENLLD	SDHRELIGDY	SKAFLLQTVD
bmy_hpp13.fas	YEMPEFSSDS	TMRILSNLVQ	HILKKYYGNG	TRKSPEMPVI	LEVSLEGSHD
pdb1qb0.A.-	GKHQDL....	.KYISPETMV	ALLTGKFSNIVDKFVI	VDCRYPYEYE
bmy_hpp13.fas	TANCEACTLG	ICGQGLKSCM	TKPSKSLLPH	LKTGNSSPGI	GAVYLANQAK
pdb1qb0.A.-	GGHIKTAVNL	PLERDAESFL	LKS.....P	IAPCSLDKRV	ILIFHCEFSS
bmy_hpp13.fas	NQSAEAKEAK	GSGYEKLGPS	RDPDPLNICV	FILLLVFIVV	KCFTSE....
pdb1qb0.A.-	ERGPRMCRFI	RERDRAVN..	...DYPSLYY	PEMYILKGGY	KEFFPQHHPNF
bmy_hpp13.fas	SE.....
pdb1qb0.A.-	PQHHPNFCEPQ	DYRPMNHEAF	KDELKTFRLLK	TRSWAGERSR	RELCSRLQDQ

FIG. 3B

Query	-----MRVIEGKGFQAQGL-----PDVNWIFNPGSGVPPASEVGLPPKCRFCATRTGSTG	49
Target :.:.: :.:.	
Target	MKSRRWFHPNITGVEAENLLLTRGV DGSFLARPSKS-----NPGDLTLSVRRNGAVT	52
Query	HPRVRCQKCSWSQYEMPEFSSDSTMRI LSNLVQHILKKYYGNGTRKSPEMPVILEVSLEG	109
Target	.:.::. .:.: :.:.: :.:.	
Target	HIKI QNTGDYYDLYGG-----EKFATLAE L VQYYME--HHGQLKEKNGDVIELKYPLNC	104
Query:	SHDTANCEACTLGICGQGLKSCMTKPSK SLLPHLKTGNSSPGIGAVYLANQAKNQSAEAK	169
Target	: :.:.: .: :.:. :.:.	
Target	A-DPTSERWFHGHLSGKEAEKLLTE-----KGKHGSFLVRESQS-----	142
Query:	EAKGSGYEKLGPSRDPDPLNICVFILL-----LVFIVVKCFTSE-----	208
Target	. . :.:.:.: :.:.: .:.	
Target	-----HPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGER	186
Query:	-----	208
Target	FDSLTDLVEHYKKNPMVETLGTVLQLKQPLNTRINAAEIESRVRELSKLAETTDKVKQG	246
Query:	-----	208
Target	FWEEFETLQQQECKLLYSRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNEPVSDYIN	306
Query:	-----	208
Target	ANIIMPEFETKCNNSKPKKSYIATQGCLQNTVND FWRMV FQENSRVIVMTTKEVERGKSK	366
Query:	-----	208
Target	CVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKVGQGNTERTVWQYHFRTWPDH	426
Query:	-----	208
Target	GVPSDPGGVLD FLEEVHHKQESIMDAGPVVVHCSAGIGRTGT FIVIDILIDI IREKGVDC	486
Query:	-----	208
Target	DIDVPKTIQMVR SQRS GMVQTEAQYRSIYMAVQHYIETL	525

FIG. 4

Alignment 1 Score 492.00 (Bits)

BMSPROT:AC06831 1 MRVIEGKGFAQGLPDVNWIFNP
 MRVIEGKGFAQGLPDVNWIFNP
 MRVIEGKGFAQGLPDVNWIFNP

AC068318_11 1302 aagaggagtgcgccgatatac
 tgtagagtcagtcatagttac
 ggtaaggctcattttacgcca

BMSPROT:AC06831 23 SGVPPASEVGLPP
 SGVPPASEVGLPP
 SGVPPASEVGLPP

AC068318_11 1368 GGTATGAG Intron 1 CAGGTtggccgagggccc
 <1-----[1369 : 1970]-1> cgtcccgatgtcc
 cttttccatgtgc

BMSPROT:AC06831 37 KCRFCATRTGSTGHPRV
 KCRFCATRTGSTGHPRV
 KCRFCATRTGSTGHPRV R:R[agg]

AC068318_11 2012 atattgacagaagccagAGGTGCGTA Intron 2
 aggtgccgcggcgacgt <2-----[2065 : 2090]
 gcaactcattgctatcgc

BMSPROT:AC06831 54 CQKCSWSQYEMPEFSSDSTMRIILSNLVQHILKKYY
 CQKCSWSQYEMPEFSSDSTMRIILSNLVQHILKKYY
 CQKCSWSQYEMPEFSSDSTMRIILSNLVQHILKKYY

AC068318_11 2088 AAGGtcattttctgacgtttgaaaaacaacgccacaatt
 -2> gaagcgcaaatcatccagctgttgattaattaaaa
 cggccgcagtggtgccgtccggtgccgggtaggact

BMSPROT:AC06831 90 GNGTRKSPMPVILEVSLEGSHTANCEACTLGICGQGL
 GNGTRKSPMPVILEVSLEGSHTANCEACTLGICGQGL
 GNGTRKSPMPVILEVSLEGSHTANCEACTLGICGQGL

AC068318_11 2197 gagaaatcgacgacggtcggtcgagatggtatgatgcgt
 gagcgaccatctttatctagcaaccagacgctgtggagt
 atcgggtaagaacgagcgaaactcacttgactgcctagca

BMSPROT:AC06831 129 KSCMTKPSKSLPHLKTGNSSPGIGAVYLANQAKNQSAE
 KSCMTKPSKSLPHLKTGNSSPGIGAVYLANQAKNQSAE
 KSCMTKPSKSLPHLKTGNSSPGIGAVYLANQAKNQSAE

AC068318_11 2314 aataaactatcccccaagattcgagggtcgacgaactgg
 aggtcaccacttcatacgacccgtgctatcaacaaacca
 accgaggcacacccagtgctcatatttgccacacgcgatg

BMSPROT:AC06831 168 AKEAKGSGYEKLGPSRDPDPLNICVFILLLVFIVVKCFT
 AKEAKGSGYEKLGPSRDPDPLNICVFILLLVFIVVKCFT
 AKEAKGSGYEKLGPSRDPDPLNICVFILLLVFIVVKCFT

AC068318_11 2431 gaggagagtgatgcacgcgccaatgtatccgtaggatta
 caacaggggaaatgcggacactatgttttttttttagtc
 aagtgggtgtgaagctacatagcctcttggtattacacta

BMSPROT:AC06831 207 SE
 SE
 SE

AC068318_11 2548 tg
 ca
 aa

FIG. 5

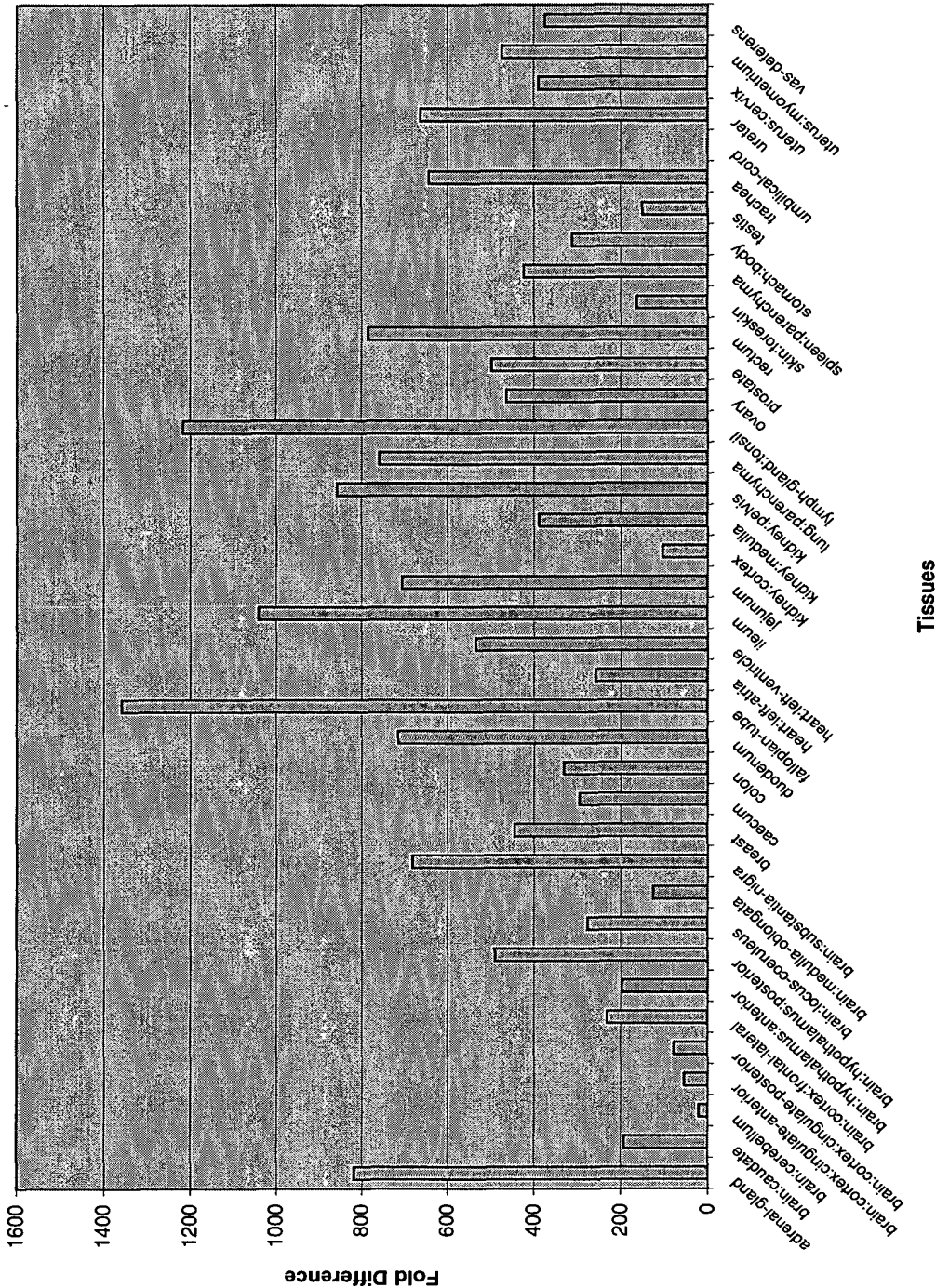


FIG. 6

Protein	Genbank ID	Identities	Similarities
Human CDC25B protein	gi NM_004358	18.1%	22.7%
Human Shp-2 protein	gi 4558224	30.0%	50.0%

FIG. 7

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1aaxA      EMEKEFEQID KSGSWAAIYQ DIRHEAS... ..DFPC RVAKLPKNKN
bmy_hpp13  .....MVV DFWTWEQTFQ ELIQEAKPRA TWTLKLDGNL QL..DCLAQG

          + ++
1aaxA      RNRYRDVSPF DHSRIKLHQE DNDYINASLI KMEEAQRSYI LTQGPLPNTC
bmy_hpp13  WKQYQQRAF. ....GW F RCSSCQRSWA SAQVQI..LC
          * *

1aaxA      GHFWEMVWEQ KSRGVVMLNR VMEKGSLKCA Q.YWPQKEEK EMIFEDTNLK
bmy_hpp13  HTYWEH...W TSQGQVRMRL FG....QRCQ KCSWSQYEMP EFSSDSTMRI

          ++
1aaxA      LTLISEDI.K SYITVRQLEL ENLTTQETRE ILHFHYTTWP DFGVPES...
bmy_hpp13  LSNLVQHILK KYYGNGTRKS P.....EMPV ILEVSLEGSH DTANCEACTL
          *

          +++++++
1aaxA      ..... PASFLNF LFKVRESGSL SPEHGPVVVH SSAGIGRSGT
bmy_hpp13  GICGQGLKSC MTKPSKSLLP HLK...TGNS SPGIGAVYLA NQAKNQSAEA
          *** **

1aaxA      FCLADTCLLL MDKRDPSV DIKKVLLEMR KFRMGLIQTA DQLRFSYLAV
bmy_hpp13  KEAKGSGYEK LGPSRDPDPL NICVFILLV FIVVKCFTSE .....

1aaxA      IEGAKFIMGD SSVQDQWKEL SHED..
bmy_hpp13  .....

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FIG. 8

